

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Fri Jun 08 19:53:52 EDT 2007

Reviewer Comments:

<210> 10

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 10

tgygayatha tgtggytnaa rac

23

The "n" at position 18 above needs explanation in the <220>-<223> section; please explain which nucleotide(s) the "n" represents. Same error in Sequences 11 through 13.

<210> 36

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (0)...(0)

<400> 36

If "PEPTIDE" is explaining "<213> Artificial Sequence," it belongs on the <223> line. Per 1.823 of the Sequence Rules, the explanation for "Artificial Sequence" or for "Unknown" goes on the <223> line. "PEPTIDE" is not a complete explanation for "Artificial Sequence." Please give source of the genetic material. Same error in Sequences 37,

39-40.

Application No: 10698597 Version No: 2.0

Input Set:

Output Set:

Started: 2007-05-18 12:03:58.977
Finished: 2007-05-18 12:04:01.102
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 125 ms
Total Warnings: 31
Total Errors: 8
No. of SeqIDs Defined: 45
Actual SeqID Count: 45

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
E 342	'n' position not defined found at POS: 18 SEQID(10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 342	'n' position not defined found at POS: 12 SEQID(11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 342	'n' position not defined found at POS: 10 SEQID(12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
E 342	'n' position not defined found at POS: 18 SEQID(13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)

Input Set:

Output Set:

Started: 2007-05-18 12:03:58.977
Finished: 2007-05-18 12:04:01.102
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 125 ms
Total Warnings: 31
Total Errors: 8
No. of SeqIDs Defined: 45
Actual SeqID Count: 45

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29) This error has occurred more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (36)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (37)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (39)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (40)

SEQUENCE LISTING

<110> Presta, Leonard G.
Shelton, David L.
Urfer, Roman

<120> Human TRK Receptors and Neurotrophic
Factor Inhibitors

<130> 39766-0033-CP2C2C1.US

<140> 10698597

<141> 2003-10-31

<150> 10/698,597

<151> 2003-10-31

<150> 09/724,524

<151> 2000-11-27

<150> 09/156,923

<151> 1998-09-18

<150> 08/359,705

<151> 1994-12-20

<150> 08/286,846

<151> 1994-08-05

<150> 08/215,139

<151> 1994-03-18

<160> 45

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3194

<212> DNA

<213> Homo sapiens

<400> 1

ggaagggtta aagaagaagc cgcaaagcgc agggaaaggcc tccccggcacg ggtgggggaa 60
agcggccgggt gcagcgcggg gacaggcact cgggctggca ctggctgcta gggatgtcgt 120
cctggataag gtggcatgga cccgccatgg cgcggctctg gggttctgc tggctggttg 180
tgggcttctg gagggccgct ttgcgcgtc ccacgtctg caaatgcagt gcctctcgga 240
tctggtgca gaccccttc cctggcatcg tggatttcc gagattggag cctaacagt 300
tagatcctga gaacatcacc gaaatttca tcgcaaacca gaaaaggta gaaatcatca 360
acgaagatga tggtaagct tatgtggac tgagaatct gacaattgtg gattctggat 420
taaaatttgt ggctcataaa gcatttctga aaaacagcaa cctgcagcac atcaatttta 480
ccgaaaccaa actgacgagt ttgtcttagga aacatttccg tcaccttgac ttgtctgaac 540
tgatcctggt gggcaatcca ttacatgct cctgtgacat tatgtggatc aagactctcc 600
aagaggctaa atccagtcca gacactcagg atttgtactg cctgaatgaa agcagcaaga 660
atattccctt ggcaaaccctg cagataccca attgtggtt gccatctgca aatctggccc 720
cacctaacct cactgtggag gaaggaaagt ctatcacatt atcctgtagt gtggcaggtg 780

atccggttcc taatatgtat tggatgttg gtaacctggt ttccaaacat atgaatgaaa 840
caagccacac acaggcgtcc ttaaggataa ctaacatttc atccgatgac agtggaaagc 900
agatctttg tgtggcgaa aatctttaga gagaagatca agattctgtc aacctcactg 960
tgcattttgc accaactatc acatttctcg aatctccaac ctcatgaccac cactggtgca 1020
ttccattcac tgtgaaaggc aacccaaaac cagcgcttca gtggttctat aacggggcaa 1080
tattgaatga gtccaaatac atctgtacta aaatacatgt taccaatcac acggagtacc 1140
acggctgcct ccagctggat aatcccactc acatgaacaa tggggactac actctaata 1200
ccaagaatga gtatggaaag gatgagaaac agatttctgc tcacttcattg ggctggctg 1260
gaattgacga tggtgaaac ccaaattatc ctgatgtaat ttatgaagat tatgaaactg 1320
cagcgaatga catcggggac accacgaaca gaagtaatga aatcccttcc acagacgtca 1380
ctgataaaac cggtcgaaac catctctcg tctatgtgt ggtgggtatt gcgtctgtgg 1440
tgggattttgc cttttggta atgctgttgc tgcttaagtt ggcaagacac tccaagtttgc 1500
gcatgaaagg cccagctcc gttatcagca atgatgatga ctctgcccgc ccactccatc 1560
acatctccaa tgggagtaac actccatctt cttcgaaagg tggcccagat gctgtcatta 1620
ttggaatgac caagatccc gtcattgaaa atccccagta ctttggcatc accaacagtc 1680
agctcaagcc agacacatTTT gttcagcaca tcaagcaca taacatgtt ctgaaaagg 1740
agcttaggcga aggacccTTT ggaaaagtgt tcctagctga atgctataac ctctgtcctg 1800
agcaggacaa gatctgggtg gcagtgaaga ccctgaagga tgccagtgc aatgcacgca 1860
aggacttcca ccgtgaggcc gagctcctga ccaacccca gcatgagcac atcgtcaagt 1920
tctatggcgt ctgcgtggag ggcgacccccc tcatcatggt cttgagttac atgaagcatg 1980
gggacctcaa caagttccctc agggcacacgc gccctgatgc cgtgctgtg gctgaggcga 2040
acccggccac ggaactgacg cagtcgcaga tgctgcataat agcccgacag atcgcgcgg 2100
gcatggctta cctggcgtcc cagcacttgc tgccacccgcga tttggccacc aggaactgccc 2160
tggtcggggaa gaacttgctg tgaaaaatcg gggactttgg gatgtcccg gacgtgtaca 2220
gcactgacta ctacagggc ggtggccaca caatgctgcc cattcgctgg atgcctccag 2280
agagcatcat gtacagggaa ttacacgacgg aaagcgcacgt ctggagccctg ggggtcggt 2340
tgtgggagat ttacacctt ggcaaaacagc cctggtacca gctgtcaaac aatgaggtga 2400
tagagtgtat cactcagggc cgagtcctgc agcgaccccg cacgtgcccc caggagggtgt 2460
atgagctgtat gctgggtgc tggcagcgcag agcccccacat gaggaagaac atcaagggca 2520
tccataccct cttcagaac ttggccaagg catctccgtt ctacctggac attcttaggt 2580
agggccctt tccccagacc gatcctccc aacgtactcc tcagacgggc tgagaggatg 2640
aacatctttt aactggcgct ggaggccacc aagctgtctt ctttcactct gacagtatta 2700
acatcaaaga ctccgagaag ctctcgaggg aagcagtgtg tacttcttca tccatagaca 2760
cagtattgac ttcttttgg cattatctct ttctctctt ccacatccc tgggtgtcc 2820
tttttctttt tttaattttt cttttcttc tttttttcg tttccctgc ttacacgattc 2880
ttacccttcc tttaaatca atctggcttc tgcattacta ttaactctgc atagacaaag 2940
gccttaacaa acgtatTTT ttatatcagc agacactcca gttgcccac cacaactaac 3000
aatgccttgt tggatgttg cttttgtatggatggatggct taagcctgtg tataaaaaaaa 3180
aaaaaaaaatc taga

3194

<210> 2
<211> 822
<212> PRT
<213> Homo sapiens

<400> 2
Met Ser Ser Trp Ile Arg Trp His Gly Pro Ala Met Ala Arg Leu Trp
1 5 10 15
Gly Phe Cys Trp Leu Val Val Gly Phe Trp Arg Ala Ala Phe Ala Cys
20 25 30
Pro Thr Ser Cys Lys Cys Ser Ala Ser Arg Ile Trp Cys Ser Asp Pro
35 40 45
Ser Pro Gly Ile Val Ala Phe Pro Arg Leu Glu Pro Asn Ser Val Asp
50 55 60
Pro Glu Asn Ile Thr Glu Ile Phe Ile Ala Asn Gln Lys Arg Leu Glu

65 70 75 80
Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr Val Gly Leu Arg Asn Leu
85 90 95
Thr Ile Val Asp Ser Gly Leu Lys Phe Val Ala His Lys Ala Phe Leu
100 105 110
Lys Asn Ser Asn Leu Gln His Ile Asn Phe Thr Arg Asn Lys Leu Thr
115 120 125
Ser Leu Ser Arg Lys His Phe Arg His Leu Asp Leu Ser Glu Leu Ile
130 135 140
Leu Val Gly Asn Pro Phe Thr Cys Ser Cys Asp Ile Met Trp Ile Lys
145 150 155 160
Thr Leu Gln Glu Ala Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys
165 170 175
Leu Asn Glu Ser Ser Lys Asn Ile Pro Leu Ala Asn Leu Gln Ile Pro
180 185 190
Asn Cys Gly Leu Pro Ser Ala Asn Leu Ala Ala Pro Asn Leu Thr Val
195 200 205
Glu Glu Gly Lys Ser Ile Thr Leu Ser Cys Ser Val Ala Gly Asp Pro
210 215 220
Val Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met
225 230 235 240
Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile Ser
245 250 255
Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn Leu Val
260 265 270
Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe Ala Pro Thr
275 280 285
Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His Trp Cys Ile Pro
290 295 300
Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu Gln Trp Phe Tyr Asn
305 310 315 320
Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile Cys Thr Lys Ile His Val
325 330 335
Thr Asn His Thr Glu Tyr His Gly Cys Leu Gln Leu Asp Asn Pro Thr
340 345 350
His Met Asn Asn Gly Asp Tyr Thr Leu Ile Ala Lys Asn Glu Tyr Gly
355 360 365
Lys Asp Glu Lys Gln Ile Ser Ala His Phe Met Gly Trp Pro Gly Ile
370 375 380
Asp Asp Gly Ala Asn Pro Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr
385 390 395 400
Gly Thr Ala Ala Asn Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn Glu
405 410 415
Ile Pro Ser Thr Asp Val Thr Asp Lys Thr Gly Arg Glu His Leu Ser
420 425 430
Val Tyr Ala Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu
435 440 445
Val Met Leu Phe Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met
450 455 460
Lys Gly Pro Ala Ser Val Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro
465 470 475 480
Leu His His Ile Ser Asn Gly Ser Asn Thr Pro Ser Ser Ser Glu Gly
485 490 495
Gly Pro Asp Ala Val Ile Ile Gly Met Thr Lys Ile Pro Val Ile Glu
500 505 510
Asn Pro Gln Tyr Phe Gly Ile Thr Asn Ser Gln Leu Lys Pro Asp Thr
515 520 525

Phe Val Gln His Ile Lys Arg His Asn Ile Val Leu Lys Arg Glu Leu
 530 535 540
 Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala Glu Cys Tyr Asn Leu
 545 550 555 560
 Cys Pro Glu Gln Asp Lys Ile Leu Val Ala Val Lys Thr Leu Lys Asp
 565 570 575
 Ala Ser Asp Asn Ala Arg Lys Asp Phe His Arg Glu Ala Glu Leu Leu
 580 585 590
 Thr Asn Leu Gln His Glu His Ile Val Lys Phe Tyr Gly Val Cys Val
 595 600 605
 Glu Gly Asp Pro Leu Ile Met Val Phe Glu Tyr Met Lys His Gly Asp
 610 615 620
 Leu Asn Lys Phe Leu Arg Ala His Gly Pro Asp Ala Val Leu Met Ala
 625 630 635 640
 Glu Gly Asn Pro Pro Thr Glu Leu Thr Gln Ser Gln Met Leu His Ile
 645 650 655
 Ala Gln Gln Ile Ala Ala Gly Met Val Tyr Leu Ala Ser Gln His Phe
 660 665 670
 Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Leu
 675 680 685
 Leu Val Lys Ile Gly Asp Phe Gly Met Ser Arg Asp Val Tyr Ser Thr
 690 695 700
 Asp Tyr Tyr Arg Val Gly Gly His Thr Met Leu Pro Ile Arg Trp Met
 705 710 715 720
 Pro Pro Glu Ser Ile Met Tyr Arg Lys Phe Thr Thr Glu Ser Asp Val
 725 730 735
 Trp Ser Leu Gly Val Val Leu Trp Glu Ile Phe Thr Tyr Gly Lys Gln
 740 745 750
 Pro Trp Tyr Gln Leu Ser Asn Asn Glu Val Ile Glu Cys Ile Thr Gln
 755 760 765
 Gly Arg Val Leu Gln Arg Pro Arg Thr Cys Pro Gln Glu Val Tyr Glu
 770 775 780
 Leu Met Leu Gly Cys Trp Gln Arg Glu Pro His Met Arg Lys Asn Ile
 785 790 795 800
 Lys Gly Ile His Thr Leu Leu Gln Asn Leu Ala Lys Ala Ser Pro Val
 805 810 815
 Tyr Leu Asp Ile Leu Gly
 820

<210> 3
 <211> 1870
 <212> DNA
 <213> Homo sapiens

<400> 3
 ggaaggttta aagaagaagc cgcaaagcgc agggaaaggcc tcccggcacg ggtgggggaa 60
 agcggccgggt gcagcgccgg gacaggcact cgggctggca ctggctgcta gggatgtcgt 120
 cctggataag gtggcatgga cccgccccatgg cgcggctctg gggcttctgc tggctgggttg 180
 tgggcttctg gagggccgct ttgcctgtc ccacgtcctg caaatgcagt gcctctcgga 240
 tctggtgcaag cgacccttct cctggcatcg tggcattcc gagatggag cctaacaatgtg 300
 tagatcctga gaacatcacc gaaaatttca tcgcaaaccg gaaaagggtt gaaatcatca 360
 acgaagatga tggtaagact tatgtggac tgagaaatct gacaattgtg gattctggat 420
 taaaatttgt ggctcataaa gcatttctga aaaacacgaa cctgcagcac atcaatttta 480
 cccgaaacaa actgacgagt ttgtcttagga aacatttccg tcaccttgac ttgtctgaac 540
 tgatcctgggt gggcaatcca ttacatgtct cctgtgacat tatgtggatc aagactctcc 600
 aagaggctaa atccagtccaa gacactcagg atttgtactg cctgaatgaa agcagcaaga 660

atatccccct ggcaaacctg cagataccca attgtggttt gccatctgca aatctggccg 720
cacctaacct cactgtggag gaaggaaagt ctatcacatt atccctgttagt gtggcagggt 780
atccgggttcc taatatgtat tgggatgttg gtaacctggt ttccaaacat atgaatgaaa 840
caagccacac acagggctcc ttaaggataa ctaacatttc atccgatgac agtgggaagc 900
agatctttg tgtggcgaa aatctttagt gagaagatca agattctgtc aacctcactg 960
tgcattttgc accaactatac acatttctcg aatctccaac ctcagaccac cactggtgca 1020
ttccattcac tgtgaaaggc aacccaaaac cagcgcctca gtggttctat aacggggcaa 1080
tattgaatga gtccaaatac atctgtacta aaatacatgt taccaatcac acggagtacc 1140
acggctgcct ccagctggat aatcccactc acatgaacaa tggggactac actctaatacg 1200
ccaagaatga gtatgggaag gatgagaac agatttctgc tcacttcatg ggctggctg 1260
gaattgacga tggtgccaaac ccaaattatc ctgatgtaat ttatgaagat tatggaactg 1320
cagcgaatga catcggggac accacgaaca gaagtaatga aatcccttcc acagacgtca 1380
ctgataaaaac cggtcgggaa catctctcg tctatgtgt ggtggtgatt gcgtctgtgg 1440
tgggattttg cctttggta atgctgttcc tgcttaagtt ggcaagacac tccaagttt 1500
gcatgaaagg ttttgggggg tttcataaga tcccactgga tgggtagctg aaataaagga 1560
aaagacagag aaagggggctg tggtgcttgt tggttatgc tgccatgtaa gctggactcc 1620
tgggactgtc gttggcttat cccggaaagt gctgcttatac tgggggttttgc tggtagatgt 1680
gggcgggttt tggaggctgt actatatgaa gcctgcataat actgtgagct gtgattgggg 1740
aacaccaatg cagaggtaac tctcaggcag ctaaggcagca cctcaagaaa acatgttaaa 1800
ttaatgccttc tcttcttaca gttagttcaaa tacaaaactg aaatgaaatc ccattggatt 1860
gtacttctct 1870

<210> 4
<211> 477
<212> PRT
<213> Home sap

<400> 4
 Met Ser Ser Trp Ile Arg Trp His Gly Pro Ala Met Ala Arg Leu Trp
 1 5 10 15
 Gly Phe Cys Trp Leu Val Val Gly Phe Trp Arg Ala Ala Phe Ala Cys
 20 25 30
 Pro Thr Ser Cys Lys Cys Ser Ala Ser Arg Ile Trp Cys Ser Asp Pro
 35 40 45
 Ser Pro Gly Ile Val Ala Phe Pro Arg Leu Glu Pro Asn Ser Val Asp
 50 55 60
 Pro Glu Asn Ile Thr Glu Ile Phe Ile Ala Asn Gln Lys Arg Leu Glu
 65 70 75 80
 Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr Val Gly Leu Arg Asn Leu
 85 90 95
 Thr Ile Val Asp Ser Gly Leu Lys Phe Val Ala His Lys Ala Phe Leu
 100 105 110
 Lys Asn Ser Asn Leu Gln His Ile Asn Phe Thr Arg Asn Lys Leu Thr
 115 120 125
 Ser Leu Ser Arg Lys His Phe Arg His Leu Asp Leu Ser Glu Leu Ile
 130 135 140
 Leu Val Gly Asn Pro Phe Thr Cys Ser Cys Asp Ile Met Trp Ile Lys
 145 150 155 160
 Thr Leu Gln Glu Ala Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys
 165 170 175
 Leu Asn Glu Ser Ser Lys Asn Ile Pro Leu Ala Asn Leu Gln Ile Pro
 180 185 190
 Asn Cys Gly Leu Pro Ser Ala Asn Leu Ala Ala Pro Asn Leu Thr Val
 195 200 205
 Glu Glu Gly Lys Ser Ile Thr Leu Ser Cys Ser Val Ala Gly Asp Pro
 210 215 220
 Val Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met

225	230	235	240												
Asn	Glu	Thr	Ser	His	Thr	Gln	Gly	Ser	Leu	Arg	Ile	Thr	Asn	Ile	Ser
245	250	255													
Ser	Asp	Asp	Ser	Gly	Lys	Gln	Ile	Ser	Cys	Val	Ala	Glu	Asn	Leu	Val
260	265	270													
Gly	Glu	Asp	Gln	Asp	Ser	Val	Asn	Leu	Thr	Val	His	Phe	Ala	Pro	Thr
275	280	285													
Ile	Thr	Phe	Leu	Glu	Ser	Pro	Thr	Ser	Asp	His	His	Trp	Cys	Ile	Pro
290	295	300													
Phe	Thr	Val	Lys	Gly	Asn	Pro	Lys	Pro	Ala	Leu	Gln	Trp	Phe	Tyr	Asn
305	310	315	320												
Gly	Ala	Ile	Leu	Asn	Glu	Ser	Lys	Tyr	Ile	Cys	Thr	Lys	Ile	His	Val
325	330	335													
Thr	Asn	His	Thr	Glu	Tyr	His	Gly	Cys	Leu	Gln	Leu	Asp	Asn	Pro	Thr
340	345	350													
His	Met	Asn	Asn	Gly	Asp	Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Glu	Tyr	Gly
355	360	365													
Lys	Asp	Glu	Lys	Gln	Ile	Ser	Ala	His	Phe	Met	Gly	Trp	Pro	Gly	Ile
370	375	380													
Asp	Asp	Gly	Ala	Asn	Pro	Asn	Tyr	Pro	Asp	Val	Ile	Tyr	Glu	Asp	Tyr
385	390	395	400												
Gly	Thr	Ala	Ala	Asn	Asp	Ile	Gly	Asp	Thr	Thr	Asn	Arg	Ser	Asn	Glu
405	410	415													
Ile	Pro	Ser	Thr	Asp	Val	Thr	Asp	Lys	Thr	Gly	Arg	Glu	His	Leu	Ser
420	425	430													
Val	Tyr	Ala	Val	Val	Val	Ile	Ala	Ser	Val	Val	Gly	Phe	Cys	Leu	Leu
435	440	445													
Val	Met	Leu	Phe	Leu	Leu	Lys	Leu	Ala	Arg	His	Ser	Lys	Phe	Gly	Met
450	455	460													
Lys	Gly	Phe	Val	Leu	Phe	His	Lys	Ile	Pro	Leu	Asp	Gly			
465	470	475													

<210> 5

<211> 2715

<212> DNA

<213> Homo sapiens

<400> 5

```
ggatccgcgt cggagatgga tgtctcttt tgcccagcca agtgttagttt ctggcgatt 60
ttcttgctgg gaagcgtctg gctggactat gtgggctccg tgctggcttg ccctgcaaat 120
tgtgtctgca gcaagactga gatcaattgc cggcggccgg acgatggaa cctcttcccc 180
ctcctggaag ggcaggattc agggAACAGC aatggAAACG ccaatatcaa catcacggac 240
atct
```